

SEQUENCE LISTING

<110> McCarthy, Sean A.

<120> NOVEL CRSP PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREFOR

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<150> 08/842,898

<151> 1997-04-17

<150> 60/071,589

<151> 1998-01-15

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<170> PatentIn Ver. 2.0

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Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Lys
65 70 75 80
Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
85 90 95
Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
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Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
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Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
130 135 140
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145 150 155 160
Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
165 170 175
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180 185 190
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
195 200 205
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240
Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

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Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu	
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Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe	
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Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu	
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Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu	
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Met Val Ala Ala Val Leu Leu Gly Leu Ser Trp Leu Cys Ser Pro
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Leu Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp
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Leu His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys
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Asn Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys
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Ala Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys
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Cys Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp
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gca acc cca ata tta gaa agg cag ctt gat gag caa gat ggc aca cat 457
Ala Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His
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Ala Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg
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aag cca agt att aag aaa tca caa ggc agg aag gga caa gag gga gaa 553
Lys Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu
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 Ser Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg
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cat ttt tgg acg aaa att tgt aag cca gtc ctt ttg gag gga cag gtc 649
 His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val
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Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala
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Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala
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Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys
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Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser
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Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
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 Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys
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 Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
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 Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp Leu
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 His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn
 35 40 45
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 Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala
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 Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys Cys
 65 70 75 80
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 Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala
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 Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala
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Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
145 150 155 160

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Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys
165 170 175

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Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
180 185 190

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Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr Ser
195 200 205

aat cgg cag cat gct cga tta aga gta tgc caa aaa ata gaa aag cta 672
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Met Met Ala Leu Gly Ala Ala
1 5

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Gly Ala Thr Arg Val Phe Val Ala Met Val Ala Ala Ala Leu Gly Gly
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His Pro Leu Leu Gly Val Ser Ala Thr Leu Asn Ser Val Leu Asn Ser
25 30 35

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Asn Ala Ile Lys Asn Leu Pro Pro Pro Leu Gly Gly Ala Ala Gly His
40 45 50 55

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Pro Gly Ser Ala Val Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly
60 65 70

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Asp Glu Glu Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly	
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Gly Asp Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys	
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Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu Asp Gly	
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Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His Thr Lys Gly	
170 175 180	
caa gaa ggt tct gtt tgt ctc cgg tca tca gac tgt gcc tca gga ttg	689
Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys Ala Ser Gly Leu	
185 190 195	
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Glu Ile Phe Gln Arg Cys Tyr Cys Gly Glu Gly Leu Ser Cys Arg Ile	
235 240 245	
cag aaa gat cac cat caa gcc agt aat tct tct agg ctt cac act tgt	881
Gln Lys Asp His His Gln Ala Ser Asn Ser Ser Arg Leu His Thr Cys	
250 255 260	
cag aga cac taaaccagct atccaaaatg cagtgaactc cttttatata	930
Gln Arg His	
265	
atagatgcta tgaaaacctt ttatgacctt catcaactca atcctaagga tatacaagtt	990
ctgtgggttc agttaagcat tccaataaca ccttccaaaa acctggagtg taagagcttt	1050

gtttctttat ggaactcccc tgtgattgca gtaaattact gtattgtaaa ttctcagtgt 1110
ggcacttacc tgtaaattgca atgaaacttt taattatattt tctaaagggtg ctgcactgcc 1170
tattttttcct cttgttatgt aaatttttgt acacattgat tgttatcttg actgacaaat 1230
attctatatt gaactgaagt aaatcatttc agcttatagt tcttaaaagc ataacccttt 1290
accccattnn attctagagt cnagaacgca aggatctctt ggaatgacaa atgataggta 1350
cctaaaatgt aacatgaaaa tactagctta ttttctgaaa tgtactatct taatgcttaa 1410
attatatttc cctttaggct gtgatagttt ttgaaataaa atttaacatt taatatcatg 1470
aaatgktata agtagacata aaaaaaaaaa aaaaaaaaaa agggcggccg ctagactag 1529

<210> 8

<211> 266

<212> PRT

<213> Homo sapiens

<400> 8

Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met
1 5 10 15

Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr
20 25 30

Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro
35 40 45

Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro
50 55 60

Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr
65 70 75 80

Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr
85 90 95

Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu
100 105 110

Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys
115 120 125

Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn
130 135 140

His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn
145 150 155 160

Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser
165 170 175

Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser
 180 185 190
 Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys
 195 200 205
 Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg
 210 215 220
 Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly
 225 230 235 240
 Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn
 245 250 255
 Ser Ser Arg Leu His Thr Cys Gln Arg His
 260 265

<210> 9
 <211> 798
 <212> DNA
 <213> Homo sapiens

<220>
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 <222> (1)..(798)

<400> 9
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 Met Met Ala Leu Gly Ala Ala Gly Ala Thr Arg Val Phe Val Ala Met
 1 5 10 15
 gta gcg gcg gct ctc ggc ggc cac cct ctg ctg gga gtg agc gcc acc 96
 Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr
 20 25 30
 ttg aac tcg gtt ctc aat tcc aac gct atc aag aac ctg ccc cca ccg 144
 Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro
 35 40 45
 ctg ggc ggc gct gcg ggg cac cca ggc tct gca gtc agc gcc gcg ccg 192
 Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro
 50 55 60
 gga atc ctg tac ccg ggc ggg aat aag tac cag acc att gac aac tac 240
 Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr
 65 70 75 80
 cag ccg tac ccg tgc gca gag gac gag gag tgc ggc act gat gag tac 288
 Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr
 85 90 95
 tgc gct agt ccc acc cgc gga ggg gac gca ggc gtg caa atc tgt ctc 336
 Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu
 100 105 110

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gcc tgc agg aag cgc cga aaa cgc tgc atg cgt cac gct atg tgc tgc 384
Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys
      115                      120                      125

ccc ggg aat tac tgc aaa aat gga ata tgc gtg tct tct gat caa aat 432
Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn
      130                      135                      140

cat ttc cga gga gaa att gag gaa acc atc act gaa agc ttt ggt aat 480
His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn
145                      150                      155                      160

gat cat agc acc ttg gat ggg tat tcc aga aga acc acc ttg tct tca 528
Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser
      165                      170                      175

aaa atg tat cac acc aaa gga caa gaa ggt tct gtt tgt ctc cgg tca 576
Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser
      180                      185                      190

tca gac tgt gcc tca gga ttg tgt tgt gct aga cac ttc tgg tcc aag 624
Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys
      195                      200                      205

atc tgt aaa cct gtc ctg aaa gaa ggt caa gtg tgt acc aag cat agg 672
Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg
      210                      215                      220

aga aaa ggc tct cat gga cta gaa ata ttc cag cgt tgt tac tgt gga 720
Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly
225                      230                      235                      240

gaa ggt ctg tct tgc cgg ata cag aaa gat cac cat caa gcc agt aat 768
Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn
      245                      250                      255

tct tct agg ctt cac act tgt cag aga cac 798
Ser Ser Arg Leu His Thr Cys Gln Arg His
      260                      265

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<210> 10
<211> 702
<212> DNA
<213> Homo sapiens

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<220>
<221> CDS
<222> (1)..(537)

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<400> 10
gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga 48
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
  1                      5                      10                      15

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tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga 96
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
                20                      25                      30

gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc 144
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
                35                      40                      45

cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt 192
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
                50                      55                      60

act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg 240
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
                65                      70                      75                      80

gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa 288
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
                85                      90                      95

ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg 336
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
                100                      105                      110

ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc 384
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
                115                      120                      125

cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg 432
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
                130                      135                      140

ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa 480
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
                145                      150                      155                      160

gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt 528
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
                165                      170                      175

cag aaa att tgatcaccat tgaggaacat catcaattgc agactgtgaa 577
Gln Lys Ile

gttgtgtatt taatgcatta tagcatggtg gaaaataagg ttcagatgca gaagaatggc 637

taaaataaga aacgtgataa gaatatagat gatcacaaaa aaaaaaaaaa aaaagatgcg 697

gccgc 702

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<210> 11
<211> 179
<212> PRT
<213> Homo sapiens

<400> 11

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Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
 1 5 10 15
 Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
 20 25 30
 Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
 35 40 45
 Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
 50 55 60
 Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
 65 70 75 80
 Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
 85 90 95
 Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
 100 105 110
 Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
 115 120 125
 His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
 130 135 140
 Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 145 150 155 160
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
 165 170 175
 Gln Lys Ile

<210> 12
 <211> 537
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(537)

<400> 12
 gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga 48
 Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
 1 5 10 15
 tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga 96
 Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
 20 25 30

gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc 144
 Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
 35 40 45

cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt 192
 Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
 50 55 60

act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg 240
 Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
 65 70 75 80

gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa 288
 Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
 85 90 95

ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg 336
 Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
 100 105 110

ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc 384
 Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
 115 120 125

cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg 432
 His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
 130 135 140

ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa 480
 Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 145 150 155 160

gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt 528
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
 165 170 175

cag aaa att
 Gln Lys Ile 537

<210> 13
 <211> 928
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (75)..(800)

<400> 13
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 agaaggggag ggggt atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg 110
 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg
 1 5 10

cat	ctg	ctg	gtc	ctg	ctg	ctg	ctc	ctc	tct	acc	ctg	gtg	atc	ccc	tcc	158
His	Leu	Leu	Val	Leu	Leu	Leu	Leu	Leu	Ser	Thr	Leu	Val	Ile	Pro	Ser	
		15					20					25				
gct	gca	gct	cct	atc	cat	gat	gct	gac	gcc	caa	gag	agc	tcc	ttg	ggc	206
Ala	Ala	Ala	Pro	Ile	His	Asp	Ala	Asp	Ala	Gln	Glu	Ser	Ser	Leu	Gly	
		30				35					40					
ctc	aca	ggc	ctc	cag	agc	cta	ctc	caa	ggc	ttc	agc	cga	ctt	ttc	ctg	254
Leu	Thr	Gly	Leu	Gln	Ser	Leu	Leu	Gln	Gly	Phe	Ser	Arg	Leu	Phe	Leu	
	45				50					55					60	
aaa	ggc	aac	ctg	ctt	cgg	ggc	ata	gac	agc	tta	ttc	tct	gcc	ccc	atg	302
Lys	Gly	Asn	Leu	Leu	Arg	Gly	Ile	Asp	Ser	Leu	Phe	Ser	Ala	Pro	Met	
				65				70						75		
gac	ttc	cgg	ggc	ctc	cct	ggg	aac	tac	cac	aaa	gag	gag	aac	cag	gag	350
Asp	Phe	Arg	Gly	Leu	Pro	Gly	Asn	Tyr	His	Lys	Glu	Glu	Asn	Gln	Glu	
			80					85					90			
cac	cag	ctg	ggg	aac	aac	acc	ctc	tcc	agc	cac	ctc	cag	atc	gac	aag	398
His	Gln	Leu	Gly	Asn	Asn	Thr	Leu	Ser	Ser	His	Leu	Gln	Ile	Asp	Lys	
		95					100					105				
atg	acc	gac	aac	aag	aca	gga	gag	gtg	ctg	atc	tcc	gag	aat	gtg	gtg	446
Met	Thr	Asp	Asn	Lys	Thr	Gly	Glu	Val	Leu	Ile	Ser	Glu	Asn	Val	Val	
	110					115					120					
gca	tcc	att	caa	cca	gcg	gag	ggg	agc	ttc	gag	ggc	gat	ttg	aag	gta	494
Ala	Ser	Ile	Gln	Pro	Ala	Glu	Gly	Ser	Phe	Glu	Gly	Asp	Leu	Lys	Val	
	125				130				135					140		
ccc	agg	atg	gag	gag	aag	gag	gcc	ctg	gta	ccc	atc	cag	aag	gcc	acg	542
Pro	Arg	Met	Glu	Glu	Lys	Glu	Ala	Leu	Val	Pro	Ile	Gln	Lys	Ala	Thr	
				145				150						155		
gac	agc	ttc	cac	aca	gaa	ctc	cat	ccc	cgg	gtg	gcc	ttc	tgg	atc	att	590
Asp	Ser	Phe	His	Thr	Glu	Leu	His	Pro	Arg	Val	Ala	Phe	Trp	Ile	Ile	
			160					165					170			
aag	ctg	cca	cgg	cgg	agg	tcc	cac	cag	gat	gcc	ctg	gag	ggc	ggc	cac	638
Lys	Leu	Pro	Arg	Arg	Arg	Ser	His	Gln	Asp	Ala	Leu	Glu	Gly	Gly	His	
		175					180					185				
tgg	ctc	agc	gag	aag	cga	cac	cgc	ctg	cag	gcc	atc	cgg	gat	gga	ctc	686
Trp	Leu	Ser	Glu	Lys	Arg	His	Arg	Leu	Gln	Ala	Ile	Arg	Asp	Gly	Leu	
	190					195					200					
cgc	aag	ggg	acc	cac	aag	gac	gtc	cta	gaa	gag	ggg	acc	gag	agc	tcc	734
Arg	Lys	Gly	Thr	His	Lys	Asp	Val	Leu	Glu	Glu	Gly	Thr	Glu	Ser	Ser	
	205				210				215						220	
tcc	cac	tcc	agg	ctg	tcc	ccc	cga	aag	acc	cac	tta	ctg	tac	atc	ctc	782
Ser	His	Ser	Arg	Leu	Ser	Pro	Arg	Lys	Thr	His	Leu	Leu	Tyr	Ile	Leu	
				225				230						235		

agg ccc tct cgg cag ctg taggggtggg gaccggggag cacctgcctg 830
Arg Pro Ser Arg Gln Leu
240

tagcccccat cagaccctgc cccaagcacc atatggaaat aaagttcttt cttacatcta 890
aaaaaaaaa aaaaaaaaaa aaaaaaattg gcggccgc 928

<210> 14
<211> 242
<212> PRT
<213> Homo sapiens

<400> 14
Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
1 5 10 15
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
20 25 30
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
35 40 45
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
50 55 60
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
65 70 75 80
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
85 90 95
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
100 105 110
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
115 120 125
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
130 135 140
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
145 150 155 160
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
165 170 175
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu
180 185 190
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
195 200 205
His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg
210 215 220

Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
 225 230 235 240

Gln Leu

<210> 15
 <211> 726
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(726)

<400> 15
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 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
 1 5 10 15
 ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct gca gct cct 96
 Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Pro
 20 25 30
 atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc aca ggc ctc 144
 Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
 35 40 45
 cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa ggt aac ctg 192
 Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
 50 55 60
 ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac ttc cgg ggc 240
 Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
 65 70 75 80
 ctc cct ggg aac tac cac aaa gag gag aac cag gag cac cag ctg ggg 288
 Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
 85 90 95
 aac aac acc ctc tcc agc cac ctc cag atc gac aag atg acc gac aac 336
 Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
 100 105 110
 aag aca gga gag gtg ctg atc tcc gag aat gtg gtg gca tcc att caa 384
 Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
 115 120 125
 cca gcg gag ggg agc ttc gag ggt gat ttg aag gta ccc agg atg gag 432
 Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
 130 135 140
 gag aag gag gcc ctg gta ccc atc cag aag gcc acg gac agc ttc cac 480
 Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
 145 150 155 160

aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att aag ctg cca cgg 528
 Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
 165 170 175

cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac tgg ctc agc gag 576
 Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu
 180 185 190

aag cga cac cgc ctg cag gcc atc cgg gat gga ctc cgc aag ggg acc 624
 Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
 195 200 205

cac aag gac gtc cta gaa gag ggg acc gag agc tcc tcc cac tcc agg 672
 His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg
 210 215 220

ctg tcc ccc cga aag acc cac tta ctg tac atc ctc agg ccc tct cgg 720
 Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
 225 230 235 240

cag ctg
 Gln Leu 726

<210> 16
 <211> 2381
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (110)..(1156)

<400> 16
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 agctcagctt tgttcattcg aattgggcgg cggccagcgc ggaacaaac atg cag cgg 118
 Met Gln Arg
 1

ctc ggg ggt att ttg ctg tgt aca ctg ctg gcg gcg gcg gtc ccc act 166
 Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala Val Pro Thr
 5 10 15

gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg gag ccg ggc 214
 Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala Glu Pro Gly
 20 25 30 35

cca gct ctc aac tac cct cag gag gaa gct acg ctc aat gag atg ttt 262
 Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe
 40 45 50

cga gag gtg gag gag ctg atg gaa gac act cag cac aaa ctg cgc agt 310
 Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser
 55 60 65

gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa acg tcc tct	358
Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Thr Ser Ser	
70 75 80	
gag gtg aac ctg gca agc tta cct ccc aac tat cac aat gag acc agc	406
Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn Glu Thr Ser	
85 90 95	
acg gag acc agg gtg gga aat aac aca gtc cat gtg cac cag gaa gtt	454
Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His Gln Glu Val	
100 105 110 115	
cac aag ata acc aac aac cag agt gga cag gtg gtc ttt tct gag aca	502
His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe Ser Glu Thr	
120 125 130	
gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc cat gaa tgt	550
Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser His Glu Cys	
135 140 145	
atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag ttc tcc agc	598
Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln Phe Ser Ser	
150 155 160	
ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg cta tgc acc	646
Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met Leu Cys Thr	
165 170 175	
cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg ggt cac tgc	694
Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp Gly His Cys	
180 185 190 195	
acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt gac aac cag	742
Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys Asp Asn Gln	
200 205 210	
agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga ggc ctg ctg	790
Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu	
215 220 225	
ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc tgc cat gac	838
Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp	
230 235 240	
ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg gag cct gaa	886
Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Glu	
245 250 255	
gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta tgc cag cca	934
Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro	
260 265 270 275	
cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc gtg ggc agc	982
His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe Val Gly Ser	
280 285 290	

cat gac cac agt gag gag agc cag ctg ccc agg gag gcc ccg gat gag 1030
His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala Pro Asp Glu
295 300 305

tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag ctg gaa gac 1078
Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu Leu Glu Asp
310 315 320

ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg cct gcc cct 1126
Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly Pro Ala Pro
325 330 335

gtg gag tca cta ggc gga gag gag gag att taggcccaga cccagctgag 1176
Val Glu Ser Leu Gly Gly Glu Glu Glu Ile
340 345

tcactggtag atgtgcaata gaaatggcta atttattttc ccaggagtgt ccccaagtgt 1236

ggaatggccg cagctccttc ccagtagctt ttctctctggc ttgacaaggt acagtgcagt 1296

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atttgtttga agggagagga tgggaagggg tgaagtctgc tcatgatgga tttgggggat 1476

acagggagga ggatgcctgc cttgcagacg tggacttggc aaaatgtaac ctttgctttt 1536

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gaaagttgca cacatttgta taagcatgcc tttctcctga gttttaaatt atatgtatac 2256

acaaacatgt ggccctcaaa gatcatgcac aaaccaactac tctttgctaa ttcttggact 2316

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<212> PRT
<213> Homo sapiens

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20 25 30
Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80
Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
85 90 95
Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
100 105 110
Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe
115 120 125
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser
130 135 140
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln
145 150 155 160
Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met
165 170 175
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp
180 185 190
Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys
195 200 205
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240
Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe
275 280 285

Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala
290 295 300

Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly
325 330 335

Pro Ala Pro Val Glu Ser Leu Gly Gly Glu Glu Glu Ile
340 345

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gtc ccc act gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg 96
Val Pro Thr Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala
20 25 30

gag ccg ggc cca gct ctc aac tac cct cag gag gaa gct acg ctc aat 144
Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45

gag atg ttt cga gag gtg gag gag ctg atg gaa gac act cag cac aaa 192
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60

ctg cgc agt gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa 240
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80

acg tcc tct gag gtg aac ctg gca agc tta cct ccc aac tat cac aat 288
Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
85 90 95

gag acc agc acg gag acc agg gtg gga aat aac aca gtc cat gtg cac 336
Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
100 105 110

cag gaa gtt cac aag ata acc aac aac cag agt gga cag gtg gtc ttt Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe 115 120 125	384
tct gag aca gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser 130 135 140	432
cat gaa tgt atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln 145 150 155 160	480
ttc tcc agc ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met 165 170 175	528
cta tgc acc cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp 180 185 190	576
ggc cac tgc acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys 195 200 205	624
gac aac cag agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg 210 215 220	672
ggc ctg ctg ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu 225 230 235 240	720
tgc cat gac ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu 245 250 255	768
gag cct gaa gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu 260 265 270	816
tgc cag cca cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe 275 280 285	864
gtg ggc agc cat gac cac agt gag gag agc cag ctg ccc agg gag gcc Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala 290 295 300	912
ccg gat gag tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu 305 310 315 320	960
ctg gaa gac ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg Leu Glu Asp Leu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly 325 330 335	1008

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Pro Ala Pro Val Glu Ser Leu Gly Gly Glu Glu Glu Ile
340 345

1047

<210> 19

<211> 8

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<213> synthtic construct

<400> 19

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

SEQUENCE LISTING

<110> McCarthy, Sean A.

<120> NOVEL CRSP PROTEIN AND NUCLEIC ACID MOLECULES AND USES THEREFOR

<130> MEI-008

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<150> 08/842,898

<151> 1997-04-17

<150> 60/071,589

<151> 1998-01-15

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<210> 1

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<212> DNA

<213> Homo sapiens

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<222> (38)..(1087)

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1 5

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Thr Leu Leu Cys Leu Leu Leu Ala Ala Ala Val Pro Thr Ala Pro Ala
10 15 20

ccc gct ccg acg gcg acc tcg gct cca gtc aag ccc ggc ccg gct ctc 151
Pro Ala Pro Thr Ala Thr Ser Ala Pro Val Lys Pro Gly Pro Ala Leu
25 30 35

agc tac ccg cag gag gag gcc acc ctc aat gag atg ttc cgc gag gtt 199
Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe Arg Glu Val
40 45 50

gag gaa ctg atg gag gac acg cag cac aaa ttg cgc agc gcg gtg gaa 247
Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser Ala Val Glu
55 60 65 70

gag atg gag gca gaa gaa gct gct gct aaa gca tca tca gaa gtg aac 295
Glu Met Glu Ala Glu Glu Ala Ala Ala Lys Ala Ser Ser Glu Val Asn
75 80 85

ctg gca aac tta cct ccc agc tat cac aat gag acc aac aca gac acg	343
Leu Ala Asn Leu Pro Pro Ser Tyr His Asn Glu Thr Asn Thr Asp Thr	
90 95 100	
aac gtt gga aat aat acc atc cat gtg cac cga gaa att cac aag ata	391
Asn Val Gly Asn Asn Thr Ile His Val His Arg Glu Ile His Lys Ile	
105 110 115	
acc aac aac cag act gga caa atg gtc ttt tca gag aca gtt atc aca	439
Thr Asn Asn Gln Thr Gly Gln Met Val Phe Ser Glu Thr Val Ile Thr	
120 125 130	
tct gtg gga gac gaa gaa ggc aga agg agc cac gag tgc atc atc gac	487
Ser Val Gly Asp Glu Glu Gly Arg Arg Ser His Glu Cys Ile Ile Asp	
135 140 145 150	
gag gac tgt ggg ccc agc atg tac tgc cag ttt gcc agc ttc cag tac	535
Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln Phe Ala Ser Phe Gln Tyr	
155 160 165	
acc tgc cag cca tgc cgg ggc cag agg atg ctc tgc acc cgg gac agt	583
Thr Cys Gln Pro Cys Arg Gly Gln Arg Met Leu Cys Thr Arg Asp Ser	
170 175 180	
gag tgc tgt gga gac cag ctg tgt gtc tgg ggt cac tgc acc aaa atg	631
Glu Cys Cys Gly Asp Gln Leu Cys Val Trp Gly His Cys Thr Lys Met	
185 190 195	
gcc acc agg ggc agc aat ggg acc atc tgt gac aac cag agg gac tgc	679
Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys Asp Asn Gln Arg Asp Cys	
200 205 210	
cag ccg ggg ctg tgc tgt gcc ttc cag aga ggc ctg ctg ttc cct gtg	727
Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu Phe Pro Val	
215 220 225 230	
tgc aca ccc ctg ccc gtg gag ggc gag ctt tgc cat gac ccc gcc agc	775
Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp Pro Ala Ser	
235 240 245	
cgg ctt ctg gac ctc atc acc tgg gag cta gag cct gat gga gcc ttg	823
Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Asp Gly Ala Leu	
250 255 260	
gac cga tgc cct tgt gcc agt ggc ctc ctc tgc cag ccc cac agc cac	871
Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro His Ser His	
265 270 275	
agc ctg gtg tat gtg tgc aag ccg acc ttc gtg ggg agc cgt gac caa	919
Ser Leu Val Tyr Val Cys Lys Pro Thr Phe Val Gly Ser Arg Asp Gln	
280 285 290	
gat ggg gag atc ctg ctg ccc aga gag gtc ccc gat gag tat gaa gtt	967
Asp Gly Glu Ile Leu Leu Pro Arg Glu Val Pro Asp Glu Tyr Glu Val	
295 300 305 310	

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 Gly Ser Phe Met Glu Glu Val Arg Gln Glu Leu Glu Asp Leu Glu Arg
 315 320 325
 agc ctg act gaa gag atg gcg ctg agg gag cct gcg gct gcc gcc gct 1063
 Ser Leu Thr Glu Glu Met Ala Leu Arg Glu Pro Ala Ala Ala Ala
 330 335 340
 gca ctg ctg gga agg gaa gag att tagatctgga ccaggctgtg ggtagatgtg 1117
 Ala Leu Leu Gly Arg Glu Glu Ile
 345 350
 caatagaaat agctaattta tttccccang tgtgtgcttt aagcgtgggc tgaccaggct 1177
 tcttctaca tcttcttccc agtaagtttc cctcttggtc tgacagcatg aggtgtttgtg 1237
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 cgaacactga actctacgcc actccacaaa tgatgttttc aggtgtcatg gactgttgcc 2317
 accatgtatt catccagagt tcttaaagtt taaagttgca catgattgta taagcatgct 2377
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<212> PRT
<213> Homo sapiens

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Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80
Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
85 90 95
Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
100 105 110
Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe
115 120 125
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser
130 135 140
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln
145 150 155 160
Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met
165 170 175
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp
180 185 190
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys
195 200 205
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240
Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe
275 280 285

Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val
290 295 300

Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu
325 330 335

Pro Ala Ala Ala Ala Ala Ala Leu Leu Gly Arg Glu Glu Ile
340 345 350

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gtc ccc acg gcc ccc gcg ccc gct ccg acg gcg acc tcg gct cca gtc 96
Val Pro Thr Ala Pro Ala Pro Ala Pro Thr Ala Thr Ser Ala Pro Val
20 25 30

aag ccc ggc ccg gct ctc agc tac ccg cag gag gag gcc acc ctc aat 144
Lys Pro Gly Pro Ala Leu Ser Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45

gag atg ttc cgc gag gtt gag gaa ctg atg gag gac acg cag cac aaa 192
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60

ttg cgc agc gcg gtg gaa gag atg gag gca gaa gaa gct gct gct aaa 240
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80

gca tca tca gaa gtg aac ctg gca aac tta cct ccc agc tat cac aat 288
Ala Ser Ser Glu Val Asn Leu Ala Asn Leu Pro Pro Ser Tyr His Asn
85 90 95

gag acc aac aca gac acg aac gtt gga aat aat acc atc cat gtg cac 336
Glu Thr Asn Thr Asp Thr Asn Val Gly Asn Asn Thr Ile His Val His
100 105 110

cga gaa att cac aag ata acc aac aac cag act gga caa atg gtc ttt	384
Arg Glu Ile His Lys Ile Thr Asn Asn Gln Thr Gly Gln Met Val Phe	
115 120 125	
tca gag aca gtt atc aca tct gtg gga gac gaa gaa ggc aga agg agc	432
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Arg Arg Ser	
130 135 140	
cac gag tgc atc atc gac gag gac tgt ggg ccc agc atg tac tgc cag	480
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Ser Met Tyr Cys Gln	
145 150 155 160	
ttt gcc agc ttc cag tac acc tgc cag cca tgc cgg ggc cag agg atg	528
Phe Ala Ser Phe Gln Tyr Thr Cys Gln Pro Cys Arg Gly Gln Arg Met	
165 170 175	
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Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Val Trp	
180 185 190	
ggt cac tgc acc aaa atg gcc acc agg ggc agc aat ggg acc atc tgt	624
Gly His Cys Thr Lys Met Ala Thr Arg Gly Ser Asn Gly Thr Ile Cys	
195 200 205	
gac aac cag agg gac tgc cag ccg ggg ctg tgc tgt gcc ttc cag aga	672
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg	
210 215 220	
ggc ctg ctg ttc cct gtg tgc aca ccc ctg ccc gtg gag ggc gag ctt	720
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu	
225 230 235 240	
tgc cat gac ccc gcc agc cgg ctt ctg gac ctc atc acc tgg gag cta	768
Cys His Asp Pro Ala Ser Arg Leu Leu Asp Leu Ile Thr Trp Glu Leu	
245 250 255	
gag cct gat gga gcc ttg gac cga tgc cct tgt gcc agt ggc ctc ctc	816
Glu Pro Asp Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu	
260 265 270	
tgc cag ccc cac agc cac agc ctg gtg tat gtg tgc aag ccg acc ttc	864
Cys Gln Pro His Ser His Ser Leu Val Tyr Val Cys Lys Pro Thr Phe	
275 280 285	
gtg ggg agc cgt gac caa gat ggg gag atc ctg ctg ccc aga gag gtc	912
Val Gly Ser Arg Asp Gln Asp Gly Glu Ile Leu Leu Pro Arg Glu Val	
290 295 300	
ccc gat gag tat gaa gtt ggc agc ttc atg gag gag gtg cgc cag gag	960
Pro Asp Glu Tyr Glu Val Gly Ser Phe Met Glu Glu Val Arg Gln Glu	
305 310 315 320	
ctg gag gac ctg gag agg agc ctg act gaa gag atg gcg ctg agg gag	1008
Leu Glu Asp Leu Glu Arg Ser Leu Thr Glu Glu Met Ala Leu Arg Glu	
325 330 335	

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340 345 350

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<222> (125)..(796)

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aagg atg gtg gcg gcc gtc ctg ctg ggg ctg agc tgg ctc tgc tct ccc 169
Met Val Ala Ala Val Leu Leu Gly Leu Ser Trp Leu Cys Ser Pro
1 5 10 15
ctg gga gct ctg gtc ctg gac ttc aac aac atc agg agc tct gct gac 217
Leu Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp
20 25 30
ctg cat ggg gcc cgg aag ggc tca cag tgc ctg tct gac acg gac tgc 265
Leu His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys
35 40 45
aat acc aga aag ttc tgc ctc cag ccc cgc gat gag aag ccg ttc tgt 313
Asn Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys
50 55 60
gct aca tgt cgt ggg ttg cgg agg agg tgc cag cga gat gcc atg tgc 361
Ala Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys
65 70 75
tgc cct ggg aca ctc tgt gtg aac gat gtt tgt act acg atg gaa gat 409
Cys Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp
80 85 90 95
gca acc cca ata tta gaa agg cag ctt gat gag caa gat ggc aca cat 457
Ala Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His
100 105 110
gca gaa gga aca act ggg cac cca gtc cag gaa aac caa ccc aaa agg 505
Ala Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg
115 120 125
aag cca agt att aag aaa tca caa ggc agg aag gga caa gag gga gaa 553
Lys Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu
130 135 140

agt tgt ctg aga act ttt gac tgt ggc cct gga ctt tgc tgt gct cgt 601
 Ser Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg
 145 150 155

cat ttt tgg acg aaa att tgt aag cca gtc ctt ttg gag gga cag gtc 649
 His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val
 160 165 170 175

tgc tcc aga aga ggg cat aaa gac act gct caa gct cca gaa atc ttc 697
 Cys Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe
 180 185 190

cag cgt tgc gac tgt ggc cct gga cta ctg tgt cga agc caa ttg acc 745
 Gln Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr
 195 200 205

agc aat cgg cag cat gct cga tta aga gta tgc caa aaa ata gaa aag 793
 Ser Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys
 210 215 220

cta taaatatttc aaaataaaga agaatccaca ttgcaaaaaa aaaaaaaaaa aa 848
 Leu

<210> 5

<211> 224

<212> PRT

<213> Homo sapiens

<400> 5

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 1 5 10 15

Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp Leu
 20 25 30

His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn
 35 40 45

Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala
 50 55 60

Thr Cys Arg Gly Leu Arg Arg Arg Cys Gln Arg Asp Ala Met Cys Cys
 65 70 75 80

Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala
 85 90 95

Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala
 100 105 110

Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys
 115 120 125

Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser
 130 135 140

Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
145 150 155 160

Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys
165 170 175

Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
180 185 190

Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr Ser
195 200 205

Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys Leu
210 215 220

<210> 6

<211> 672

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) .. (672)

<400> 6

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Met Val Ala Ala Val Leu Leu Gly Leu Ser Trp Leu Cys Ser Pro Leu
1 5 10 15

gga gct ctg gtc ctg gac ttc aac aac atc agg agc tct gct gac ctg 96
Gly Ala Leu Val Leu Asp Phe Asn Asn Ile Arg Ser Ser Ala Asp Leu
20 25 30

cat ggg gcc cgg aag ggc tca cag tgc ctg tct gac acg gac tgc aat 144
His Gly Ala Arg Lys Gly Ser Gln Cys Leu Ser Asp Thr Asp Cys Asn
35 40 45

acc aga aag ttc tgc ctc cag ccc cgc gat gag aag ccg ttc tgt gct 192
Thr Arg Lys Phe Cys Leu Gln Pro Arg Asp Glu Lys Pro Phe Cys Ala
50 55 60

aca tgt cgt ggg ttg cgg agg agg tgc cag cga gat gcc atg tgc tgc 240
Thr Cys Arg Gly Leu Arg Arg Cys Gln Arg Asp Ala Met Cys Cys
65 70 75 80

cct ggg aca ctc tgt gtg aac gat gtt tgt act acg atg gaa gat gca 288
Pro Gly Thr Leu Cys Val Asn Asp Val Cys Thr Thr Met Glu Asp Ala
85 90 95

acc cca ata tta gaa agg cag ctt gat gag caa gat ggc aca cat gca 336
Thr Pro Ile Leu Glu Arg Gln Leu Asp Glu Gln Asp Gly Thr His Ala
100 105 110

gaa gga aca act ggg cac cca gtc cag gaa aac caa ccc aaa agg aag 384
Glu Gly Thr Thr Gly His Pro Val Gln Glu Asn Gln Pro Lys Arg Lys
115 120 125

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cca agt att aag aaa tca caa ggc agg aag gga caa gag gga gaa agt 432
Pro Ser Ile Lys Lys Ser Gln Gly Arg Lys Gly Gln Glu Gly Glu Ser
      130                135                140

tgt ctg aga act ttt gac tgt ggc cct gga ctt tgc tgt gct cgt cat 480
Cys Leu Arg Thr Phe Asp Cys Gly Pro Gly Leu Cys Cys Ala Arg His
145                150                155                160

ttt tgg acg aaa att tgt aag cca gtc ctt ttg gag gga cag gtc tgc 528
Phe Trp Thr Lys Ile Cys Lys Pro Val Leu Leu Glu Gly Gln Val Cys
      165                170                175

tcc aga aga ggg cat aaa gac act gct caa gct cca gaa atc ttc cag 576
Ser Arg Arg Gly His Lys Asp Thr Ala Gln Ala Pro Glu Ile Phe Gln
      180                185                190

cgt tgc gac tgt ggc cct gga cta ctg tgt cga agc caa ttg acc agc 624
Arg Cys Asp Cys Gly Pro Gly Leu Leu Cys Arg Ser Gln Leu Thr Ser
      195                200                205

aat cgg cag cat gct cga tta aga gta tgc caa aaa ata gaa aag cta 672
Asn Arg Gln His Ala Arg Leu Arg Val Cys Gln Lys Ile Glu Lys Leu
      210                215                220

<210> 7
<211> 1529
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (93) .. (890)

<400> 7
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ctctttcttt ctccctcttg agtccttctg ag atg atg gct ctg ggc gca gcg 113
Met Met Ala Leu Gly Ala Ala
      1                5

gga gct acc cgg gtc ttt gtc gcg atg gta gcg gcg gct ctc gcg ggc 161
Gly Ala Thr Arg Val Phe Val Ala Met Val Ala Ala Ala Leu Gly Gly
      10                15                20

cac cct ctg ctg gga gtg agc gcc acc ttg aac tcg gtt ctc aat tcc 209
His Pro Leu Leu Gly Val Ser Ala Thr Leu Asn Ser Val Leu Asn Ser
      25                30                35

aac gct atc aag aac ctg ccc cca ccg ctg ggc ggc gct gcg ggg cac 257
Asn Ala Ile Lys Asn Leu Pro Pro Pro Leu Gly Gly Ala Ala Gly His
      40                45                50                55

cca ggc tct gca gtc agc gcc gcg ccg gga atc ctg tac ccg ggc ggg 305
Pro Gly Ser Ala Val Ser Ala Ala Pro Gly Ile Leu Tyr Pro Gly Gly
      60                65                70

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aat aag tac cag acc att gac aac tac cag ccg tac ccg tgc gca gag	353
Asn Lys Tyr Gln Thr Ile Asp Asn Tyr Gln Pro Tyr Pro Cys Ala Glu	
75 80 85	
gac gag gag tgc ggc act gat gag tac tgc gct agt ccc acc cgc gga	401
Asp Glu Glu Cys Gly Thr Asp Glu Tyr Cys Ala Ser Pro Thr Arg Gly	
90 95 100	
ggg gac gca ggc gtg caa atc tgt ctc gcc tgc agg aag cgc cga aaa	449
Gly Asp Ala Gly Val Gln Ile Cys Leu Ala Cys Arg Lys Arg Arg Lys	
105 110 115	
cgc tgc atg cgt cac gct atg tgc tgc ccc ggg aat tac tgc aaa aat	497
Arg Cys Met Arg His Ala Met Cys Cys Pro Gly Asn Tyr Cys Lys Asn	
120 125 130 135	
gga ata tgc gtg tct tct gat caa aat cat ttc cga gga gaa att gag	545
Gly Ile Cys Val Ser Ser Asp Gln Asn His Phe Arg Gly Glu Ile Glu	
140 145 150	
gaa acc atc act gaa agc ttt ggt aat gat cat agc acc ttg gat ggg	593
Glu Thr Ile Thr Glu Ser Phe Gly Asn Asp His Ser Thr Leu Asp Gly	
155 160 165	
tat tcc aga aga acc acc ttg tct tca aaa atg tat cac acc aaa gga	641
Tyr Ser Arg Arg Thr Thr Leu Ser Ser Lys Met Tyr His Thr Lys Gly	
170 175 180	
caa gaa ggt tct gtt tgt ctc cgg tca tca gac tgt gcc tca gga ttg	689
Gln Glu Gly Ser Val Cys Leu Arg Ser Ser Asp Cys Ala Ser Gly Leu	
185 190 195	
tgt tgt gct aga cac ttc tgg tcc aag atc tgt aaa cct gtc ctg aaa	737
Cys Cys Ala Arg His Phe Trp Ser Lys Ile Cys Lys Pro Val Leu Lys	
200 205 210 215	
gaa ggt caa gtg tgt acc aag cat agg aga aaa ggc tct cat gga cta	785
Glu Gly Gln Val Cys Thr Lys His Arg Arg Lys Gly Ser His Gly Leu	
220 225 230	
gaa ata ttc cag cgt tgt tac tgt gga gaa ggt ctg tct tgc cgg ata	833
Glu Ile Phe Gln Arg Cys Tyr Cys Gly Glu Gly Leu Ser Cys Arg Ile	
235 240 245	
cag aaa gat cac cat caa gcc agt aat tct tct agg ctt cac act tgt	881
Gln Lys Asp His His Gln Ala Ser Asn Ser Ser Arg Leu His Thr Cys	
250 255 260	
cag aga cac taaaccagct atccaaaatg cagtgaactc cttttatata	930
Gln Arg His	
265	
atagatgcta tgaaaacctt ttatgacctt catcaactca atcctaagga tatacaagtt	990
ctgtgggttc agttaagcat tccaataaca ccttccaaaa acctggagtg taagagcttt	1050

gtttctttat ggaactcccc tgtgattgca gtaaattact gtattgtaaa ttctcagtgt 1110
 ggcacttacc tgtaaattgca atgaaacttt taattatttt tctaaagggtg ctgcactgcc 1170
 tatttttctt cttgttatgt aaatttttgt acacattgat tggtatcttg actgacaaat 1230
 attctatatt gaactgaagt aaatcatttc agcttatagt tcttaaaagc ataacccttt 1290
 accccatttn attctagagt cnagaacgca aggatctctt ggaatgacaa atgataggta 1350
 cctaaaatgt aacatgaaaa tactagctta ttttctgaaa tgtactatct taatgcttaa 1410
 attatatttc cctttagggt gtgatagttt ttgaaataaa atttaacatt taatatcatg 1470
 aaatgktata agtagacata aaaaaaaaaa aaaaaaaaaa agggcggccg ctagactag 1529

<210> 8
 <211> 266
 <212> PRT
 <213> Homo sapiens

<400> 8
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 1 5 10 15
 Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr
 20 25 30
 Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro
 35 40 45
 Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro
 50 55 60
 Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr
 65 70 75 80
 Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr
 85 90 95
 Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu
 100 105 110
 Ala Cys Arg Lys Arg Arg Lys Arg Cys Met Arg His Ala Met Cys Cys
 115 120 125
 Pro Gly Asn Tyr Cys Lys Asn Gly Ile Cys Val Ser Ser Asp Gln Asn
 130 135 140
 His Phe Arg Gly Glu Ile Glu Glu Thr Ile Thr Glu Ser Phe Gly Asn
 145 150 155 160
 Asp His Ser Thr Leu Asp Gly Tyr Ser Arg Arg Thr Thr Leu Ser Ser
 165 170 175

Lys Met Tyr His Thr Lys Gly Gln Glu Gly Ser Val Cys Leu Arg Ser
180 185 190
Ser Asp Cys Ala Ser Gly Leu Cys Cys Ala Arg His Phe Trp Ser Lys
195 200 205
Ile Cys Lys Pro Val Leu Lys Glu Gly Gln Val Cys Thr Lys His Arg
210 215 220
Arg Lys Gly Ser His Gly Leu Glu Ile Phe Gln Arg Cys Tyr Cys Gly
225 230 235 240
Glu Gly Leu Ser Cys Arg Ile Gln Lys Asp His His Gln Ala Ser Asn
245 250 255
Ser Ser Arg Leu His Thr Cys Gln Arg His
260 265

<210> 9
<211> 798
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (798)

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1 5 10 15
gta gcg gcg gct ctc ggc ggc cac cct ctg ctg gga gtg agc gcc acc 96
Val Ala Ala Ala Leu Gly Gly His Pro Leu Leu Gly Val Ser Ala Thr
20 25 30
ttg aac tcg gtt ctc aat tcc aac gct atc aag aac ctg ccc cca ccg 144
Leu Asn Ser Val Leu Asn Ser Asn Ala Ile Lys Asn Leu Pro Pro Pro
35 40 45
ctg ggc ggc gct gcg ggg cac cca ggc tct gca gtc agc gcc gcg ccg 192
Leu Gly Gly Ala Ala Gly His Pro Gly Ser Ala Val Ser Ala Ala Pro
50 55 60
gga atc ctg tac ccg ggc ggg aat aag tac cag acc att gac aac tac 240
Gly Ile Leu Tyr Pro Gly Gly Asn Lys Tyr Gln Thr Ile Asp Asn Tyr
65 70 75 80
cag ccg tac ccg tgc gca gag gac gag gag tgc ggc act gat gag tac 288
Gln Pro Tyr Pro Cys Ala Glu Asp Glu Glu Cys Gly Thr Asp Glu Tyr
85 90 95
tgc gct agt ccc acc cgc gga ggg gac gca ggc gtg caa atc tgt ctc 336
Cys Ala Ser Pro Thr Arg Gly Gly Asp Ala Gly Val Gln Ile Cys Leu
100 105 110

<400> 10
gaa ttc ggc acg agg gtt ggg agg tat tgc cac agt ccc cac caa gga 48
Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
1 5 10 15

tca tgc gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga	96
Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg	
20 25 30	
gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc	144
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile	
35 40 45	
cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt	192
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly	
50 55 60	
act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg	240
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu	
65 70 75 80	
gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa	288
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys	
85 90 95	
ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg	336
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly	
100 105 110	
ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc	384
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu	
115 120 125	
cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg	432
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly	
130 135 140	
ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa	480
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys	
145 150 155 160	
gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt	528
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys	
165 170 175	
cag aaa att tgatcaccat tgaggaacat catcaattgc agactgtgaa	577
Gln Lys Ile	
gttgtgtatt taatgcatta tagcatggtg gaaaataagg ttcagatgca gaagaatggc	637
taaaataaga aacgtgataa gaatatagat gatcacaaaa aaaaaaaaaa aaaagatgcg	697
gccgc	702

<210> 11
 <211> 179
 <212> PRT
 <213> Homo sapiens
 <400> 11

Glu Phe Gly Thr Arg Val Gly Arg Tyr Cys His Ser Pro His Gln Gly
 1 5 10 15
 Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
 20 25 30
 Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile
 35 40 45
 Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly
 50 55 60
 Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu
 65 70 75 80
 Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys
 85 90 95
 Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly
 100 105 110
 Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu
 115 120 125
 His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly
 130 135 140
 Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys
 145 150 155 160
 Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys
 165 170 175
 Gln Lys Ile

<210> 12
 <211> 537
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)..(537)

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 1 5 10 15
 tca tcg gcc tgc atg gtg tgt cgg aga aaa aag aag cgc tgc cac cga 96
 Ser Ser Ala Cys Met Val Cys Arg Arg Lys Lys Lys Arg Cys His Arg
 20 25 30

gat ggc atg tgc tgc ccc agt acc cgc tgc aat aat ggc atc tgt atc	144
Asp Gly Met Cys Cys Pro Ser Thr Arg Cys Asn Asn Gly Ile Cys Ile	
35 40 45	
cca gtt act gaa agc atc tta acc cct cac atc ccg gct ctg gat ggt	192
Pro Val Thr Glu Ser Ile Leu Thr Pro His Ile Pro Ala Leu Asp Gly	
50 55 60	
act cgg cac aga gat cga aac cac ggt cat tac tca aac cat gac ttg	240
Thr Arg His Arg Asp Arg Asn His Gly His Tyr Ser Asn His Asp Leu	
65 70 75 80	
gga tgg cag aat cta gga aga cca cac act aag atg tca cat ata aaa	288
Gly Trp Gln Asn Leu Gly Arg Pro His Thr Lys Met Ser His Ile Lys	
85 90 95	
ggg cat gaa gga gac ccc tgc cta cga tca tca gac tgc att gaa ggg	336
Gly His Glu Gly Asp Pro Cys Leu Arg Ser Ser Asp Cys Ile Glu Gly	
100 105 110	
ttt tgc tgt gct cgt cat ttc tgg acc aaa atc tgc aaa cca gtg ctc	384
Phe Cys Cys Ala Arg His Phe Trp Thr Lys Ile Cys Lys Pro Val Leu	
115 120 125	
cat cag ggg gaa gtc tgt acc aaa caa cgc aag aag ggt tct cat ggg	432
His Gln Gly Glu Val Cys Thr Lys Gln Arg Lys Lys Gly Ser His Gly	
130 135 140	
ctg gaa att ttc cag cgt tgc gac tgt gcg aag ggc ctg tct tgc aaa	480
Leu Glu Ile Phe Gln Arg Cys Asp Cys Ala Lys Gly Leu Ser Cys Lys	
145 150 155 160	
gta tgg aaa gat gcc acc tac tcc tcc aaa gcc aga ctc cat gtg tgt	528
Val Trp Lys Asp Ala Thr Tyr Ser Ser Lys Ala Arg Leu His Val Cys	
165 170 175	
cag aaa att	537
Gln Lys Ile	

<210> 13
 <211> 928
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (75)..(800)

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 agaaggggagc gggt atg gga gaa gcc tcc cca cct gcc ccc gca agg cgg 110
 Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg
 1 5 10

cat ctg ctg gtc ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc	158
His Leu Leu Val Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser	
15 20 25	
gct gca gct cct atc cat gat gct gac gcc caa gag agc tcc ttg ggt	206
Ala Ala Ala Pro Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly	
30 35 40	
ctc aca ggc ctc cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg	254
Leu Thr Gly Leu Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu	
45 50 55 60	
aaa ggt aac ctg ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg	302
Lys Gly Asn Leu Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met	
65 70 75	
gac ttc cgg ggc ctc cct ggg aac tac cac aaa gag gag aac cag gag	350
Asp Phe Arg Gly Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu	
80 85 90	
cac cag ctg ggg aac aac acc ctc tcc agc cac ctc cag atc gac aag	398
His Gln Leu Gly Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys	
95 100 105	
atg acc gac aac aag aca gga gag gtg ctg atc tcc gag aat gtg gtg	446
Met Thr Asp Asn Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val	
110 115 120	
gca tcc att caa cca gcg gag ggg agc ttc gag ggt gat ttg aag gta	494
Ala Ser Ile Gln Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val	
125 130 135 140	
ccc agg atg gag gag aag gag gcc ctg gta ccc atc cag aag gcc acg	542
Pro Arg Met Glu Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr	
145 150 155	
gac agc ttc cac aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att	590
Asp Ser Phe His Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile	
160 165 170	
aag ctg cca cgg cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac	638
Lys Leu Pro Arg Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His	
175 180 185	
tgg ctc agc gag aag cga cac cgc ctg cag gcc atc cgg gat gga ctc	686
Trp Leu Ser Glu Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu	
190 195 200	
cgc aag ggg acc cac aag gac gtc cta gaa gag ggg acc gag agc tcc	734
Arg Lys Gly Thr His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser	
205 210 215 220	
tcc cac tcc agg ctg tcc ccc cga aag acc cac tta ctg tac atc ctc	782
Ser His Ser Arg Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu	
225 230 235	

agg ccc tct cgg cag ctg taggggtggg gaccggggag cacctgcctg 830
Arg Pro Ser Arg Gln Leu
240

tagcccccat cagaccctgc cccaagcacc atatggaaat aaagttcttt cttacatcta 890
aaaaaaaaaa aaaaaaaaaa aaaaaaattg gcggccgc 928

<210> 14
<211> 242
<212> PRT
<213> Homo sapiens

<400> 14
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1 5 10 15
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
20 25 30
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
35 40 45
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
50 55 60
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
65 70 75 80
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
85 90 95
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
100 105 110
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
115 120 125
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
130 135 140
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
145 150 155 160
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
165 170 175
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu
180 185 190
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
195 200 205
His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg
210 215 220

Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
225 230 235 240

Gln Leu

<210> 15
<211> 726
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) .. (726)

<400> 15
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Met Gly Glu Ala Ser Pro Pro Ala Pro Ala Arg Arg His Leu Leu Val
1 5 10 15
ctg ctg ctg ctc ctc tct acc ctg gtg atc ccc tcc gct gca gct cct 96
Leu Leu Leu Leu Leu Ser Thr Leu Val Ile Pro Ser Ala Ala Ala Pro
20 25 30
atc cat gat gct gac gcc caa gag agc tcc ttg ggt ctc aca ggc ctc 144
Ile His Asp Ala Asp Ala Gln Glu Ser Ser Leu Gly Leu Thr Gly Leu
35 40 45
cag agc cta ctc caa ggc ttc agc cga ctt ttc ctg aaa ggt aac ctg 192
Gln Ser Leu Leu Gln Gly Phe Ser Arg Leu Phe Leu Lys Gly Asn Leu
50 55 60
ctt cgg ggc ata gac agc tta ttc tct gcc ccc atg gac ttc cgg ggc 240
Leu Arg Gly Ile Asp Ser Leu Phe Ser Ala Pro Met Asp Phe Arg Gly
65 70 75 80
ctc cct ggg aac tac cac aaa gag gag aac cag gag cac cag ctg ggg 288
Leu Pro Gly Asn Tyr His Lys Glu Glu Asn Gln Glu His Gln Leu Gly
85 90 95
aac aac acc ctc tcc agc cac ctc cag atc gac aag atg acc gac aac 336
Asn Asn Thr Leu Ser Ser His Leu Gln Ile Asp Lys Met Thr Asp Asn
100 105 110
aag aca gga gag gtg ctg atc tcc gag aat gtg gtg gca tcc att caa 384
Lys Thr Gly Glu Val Leu Ile Ser Glu Asn Val Val Ala Ser Ile Gln
115 120 125
cca geg gag ggg agc ttc gag ggt gat ttg aag gta ccc agg atg gag 432
Pro Ala Glu Gly Ser Phe Glu Gly Asp Leu Lys Val Pro Arg Met Glu
130 135 140
gag aag gag gcc ctg gta ccc atc cag aag gcc acg gac agc ttc cac 480
Glu Lys Glu Ala Leu Val Pro Ile Gln Lys Ala Thr Asp Ser Phe His
145 150 155 160

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aca gaa ctc cat ccc cgg gtg gcc ttc tgg atc att aag ctg cca cgg 528
Thr Glu Leu His Pro Arg Val Ala Phe Trp Ile Ile Lys Leu Pro Arg
      165                      170                      175

cgg agg tcc cac cag gat gcc ctg gag ggc ggc cac tgg ctc agc gag 576
Arg Arg Ser His Gln Asp Ala Leu Glu Gly Gly His Trp Leu Ser Glu
      180                      185                      190

aag cga cac cgc ctg cag gcc atc cgg gat gga ctc cgc aag ggg acc 624
Lys Arg His Arg Leu Gln Ala Ile Arg Asp Gly Leu Arg Lys Gly Thr
      195                      200                      205

cac aag gac gtc cta gaa gag ggg acc gag agc tcc tcc cac tcc agg 672
His Lys Asp Val Leu Glu Glu Gly Thr Glu Ser Ser Ser His Ser Arg
      210                      215                      220

ctg tcc ccc cga aag acc cac tta ctg tac atc ctc agg ccc tct cgg 720
Leu Ser Pro Arg Lys Thr His Leu Leu Tyr Ile Leu Arg Pro Ser Arg
      225                      230                      235                      240

cag ctg
Gln Leu 726

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agctcagctt tggttcattcg aattgggcgg cggccagcgc ggaacaaac atg cag cgg 118
                                Met Gln Arg
                                1

ctc ggg ggt att ttg ctg tgt aca ctg ctg gcg gcg gcg gtc ccc act 166
Leu Gly Gly Ile Leu Leu Cys Thr Leu Leu Ala Ala Ala Val Pro Thr
      5                      10                      15

gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg gag ccg ggc 214
Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala Glu Pro Gly
      20                      25                      30                      35

cca gct ctc aac tac cct cag gag gaa gct acg ctc aat gag atg ttt 262
Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn Glu Met Phe
      40                      45                      50

cga gag gtg gag gag ctg atg gaa gac act cag cac aaa ctg cgc agt 310
Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys Leu Arg Ser
      55                      60                      65

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gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa acg tcc tct Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Lys Thr Ser Ser	358
70 75 80	
gag gtg aac ctg gca agc tta cct ccc aac tat cac aat gag acc agc Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn Glu Thr Ser	406
85 90 95	
acg gag acc agg gtg gga aat aac aca gtc cat gtg cac cag gaa gtt Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His Gln Glu Val	454
100 105 110 115	
cac aag ata acc aac aac cag agt gga cag gtg gtc ttt tct gag aca His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe Ser Glu Thr	502
120 125 130	
gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc cat gaa tgt Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser His Glu Cys	550
135 140 145	
atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag ttc tcc agc Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln Phe Ser Ser	598
150 155 160	
ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg cta tgc acc Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met Leu Cys Thr	646
165 170 175	
cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg ggt cac tgc Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp Gly His Cys	694
180 185 190 195	
acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt gac aac cag Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys Asp Asn Gln	742
200 205 210	
agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga ggc ctg ctg Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg Gly Leu Leu	790
215 220 225	
ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc tgc cat gac Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu Cys His Asp	838
230 235 240	
ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg gag cct gaa Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu Glu Pro Glu	886
245 250 255	
gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta tgc cag cca Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu Cys Gln Pro	934
260 265 270 275	
cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc gtg ggc agc His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe Val Gly Ser	982
280 285 290	

cat gac cac agt gag gag agc cag ctg ccc agg gag gcc ccg gat gag 1030
His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala Pro Asp Glu
295 300 305

tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag ctg gaa gac 1078
Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu Leu Glu Asp
310 315 320

ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg cct gcc cct 1126
Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly Pro Ala Pro
325 330 335

gtg gag tca cta ggc gga gag gag gag att taggcccaga cccagctgag 1176
Val Glu Ser Leu Gly Gly Glu Glu Glu Ile
340 345

tcactggtag atgtgcaata gaaatggota atttattttc ccaggagtgt ccccaagtgt 1236

ggaatggccg cagctccttc ccagtagctt ttctcttggc ttgacaaggt acagtgcagt 1296

acatttcttc cagccgccct gcttctctga cttgggaaag acaggcatgg cgggtaaggg 1356

cagcgggtgag tcgtccctcg ctgttgctag aaacgctgtc ttgttcttca tggatggaag 1416

atttgtttga agggagagga tgggaagggg tgaagtctgc tcatgatgga tttgggggat 1476

acagggagga ggatgcctgc cttgcagacg tggacttggc aaaatgtaac ctttgctttt 1536

gtcttgccgc gctcccatgg gctgaggcag tggctacaca agagctatgc tgctctgtgg 1596

cctcccacat attcatccct gtgtttcagc tcctacctca ctgtcagcac agcccttcat 1656

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ggtcaggctg acttgcatgt ccctctaacg ttcttagcag tgtggtggac actgtcttcc 1896

accgactgct tcaatacctc tgaaagccag tgctcggagt gcagttcgtg taaattaatt 1956

tgcaggaagt atacttggt aattgtaggg ctaggattgt gaatgaaatt tgcaaagtcg 2016

cttagcaaca atggaaagcc tttctcagtc acaccagaaa gtcacaacca agccaggttg 2076

tgtagagtac agctgtgaca tacagacaga agaaggctgg gctggatgtc aggcctcaga 2136

tgacggtttc aggtgccagg aactattacc attctgtatc tatccagagt tattaaaatt 2196

gaaagttgca cacatttgta taagcatgcc tttctcctga gttttaaatt atatgtatac 2256

acaaacatgt ggccctcaaa gatcatgcac aaaccactac tctttgctaa ttcttggtgact 2316

tttctctttg attttcaata aatacaaata cccttcatgc aaaaaaaaaa aaaaagggcg 2376

gccgc 2381

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<213> Homo sapiens

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20 25 30
Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80
Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
85 90 95
Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
100 105 110
Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe
115 120 125
Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser
130 135 140
His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln
145 150 155 160
Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met
165 170 175
Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp
180 185 190
Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys
195 200 205
Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg
210 215 220
Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu
225 230 235 240
Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu
245 250 255

Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu
260 265 270

Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe
275 280 285

Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala
290 295 300

Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu
305 310 315 320

Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly
325 330 335

Pro Ala Pro Val Glu Ser Leu Gly Gly Glu Glu Glu Ile
340 345

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gtc ccc act gct cct gct cct tcc ccg acg gtc act tgg act ccg gcg 96
Val Pro Thr Ala Pro Ala Pro Ser Pro Thr Val Thr Trp Thr Pro Ala
20 25 30

gag ccg ggc cca gct ctc aac tac cct cag gag gaa gct acg ctc aat 144
Glu Pro Gly Pro Ala Leu Asn Tyr Pro Gln Glu Glu Ala Thr Leu Asn
35 40 45

gag atg ttt cga gag gtg gag gag ctg atg gaa gac act cag cac aaa 192
Glu Met Phe Arg Glu Val Glu Glu Leu Met Glu Asp Thr Gln His Lys
50 55 60

ctg cgc agt gcc gtg gag gag atg gag gcg gaa gaa gca gct gct aaa 240
Leu Arg Ser Ala Val Glu Glu Met Glu Ala Glu Glu Ala Ala Ala Lys
65 70 75 80

acg tcc tct gag gtg aac ctg gca agc tta cct ccc aac tat cac aat 288
Thr Ser Ser Glu Val Asn Leu Ala Ser Leu Pro Pro Asn Tyr His Asn
85 90 95

gag acc agc acg gag acc agg gtg gga aat aac aca gtc cat gtg cac 336
Glu Thr Ser Thr Glu Thr Arg Val Gly Asn Asn Thr Val His Val His
100 105 110

cag gaa gtt cac aag ata acc aac aac cag agt gga cag gtg gtc ttt Gln Glu Val His Lys Ile Thr Asn Asn Gln Ser Gly Gln Val Val Phe 115 120 125	384
tct gag aca gtc att aca tct gta ggg gat gaa gaa ggc aag agg agc Ser Glu Thr Val Ile Thr Ser Val Gly Asp Glu Glu Gly Lys Arg Ser 130 135 140	432
cat gaa tgt atc att gat gaa gac tgt ggg ccc acc agg tac tgc cag His Glu Cys Ile Ile Asp Glu Asp Cys Gly Pro Thr Arg Tyr Cys Gln 145 150 155 160	480
ttc tcc agc ttc aag tac acc tgc cag cca tgc cgg gac cag cag atg Phe Ser Ser Phe Lys Tyr Thr Cys Gln Pro Cys Arg Asp Gln Gln Met 165 170 175	528
cta tgc acc cga gac agt gag tgc tgt gga gac cag ctg tgt gcc tgg Leu Cys Thr Arg Asp Ser Glu Cys Cys Gly Asp Gln Leu Cys Ala Trp 180 185 190	576
ggc cac tgc acc caa aag gcc acc aaa ggt ggc aat ggg acc atc tgt Gly His Cys Thr Gln Lys Ala Thr Lys Gly Gly Asn Gly Thr Ile Cys 195 200 205	624
gac aac cag agg gat tgc cag cct ggc ctg tgt tgt gcc ttc caa aga Asp Asn Gln Arg Asp Cys Gln Pro Gly Leu Cys Cys Ala Phe Gln Arg 210 215 220	672
ggc ctg ctg ttc ccc gtg tgc aca ccc ctg ccc gtg gag gga gag ctc Gly Leu Leu Phe Pro Val Cys Thr Pro Leu Pro Val Glu Gly Glu Leu 225 230 235 240	720
tgc cat gac ccc acc agc cag ctg ctg gat ctc atc acc tgg gaa ctg Cys His Asp Pro Thr Ser Gln Leu Leu Asp Leu Ile Thr Trp Glu Leu 245 250 255	768
gag cct gaa gga gct ttg gac cga tgc ccc tgc gcc agt ggc ctc cta Glu Pro Glu Gly Ala Leu Asp Arg Cys Pro Cys Ala Ser Gly Leu Leu 260 265 270	816
tgc cag cca cac agc cac agt ctg gtg tac atg tgc aag cca gcc ttc Cys Gln Pro His Ser His Ser Leu Val Tyr Met Cys Lys Pro Ala Phe 275 280 285	864
gtg ggc agc cat gac cac agt gag gag agc cag ctg ccc agg gag gcc Val Gly Ser His Asp His Ser Glu Glu Ser Gln Leu Pro Arg Glu Ala 290 295 300	912
ccg gat gag tac gaa gat gtt ggc ttc ata ggg gaa gtg cgc cag gag Pro Asp Glu Tyr Glu Asp Val Gly Phe Ile Gly Glu Val Arg Gln Glu 305 310 315 320	960
ctg gaa gac ctg gag cgg agc cta gcc cag gag atg gca ttt gag ggg Leu Glu Asp Leu Glu Arg Ser Leu Ala Gln Glu Met Ala Phe Glu Gly 325 330 335	1008

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Pro Ala Pro Val Glu Ser Leu Gly Gly Glu Glu Glu Ile
340 345

1047

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<213> synthtic construct

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Asp Tyr Lys Asp Asp Asp Asp Lys
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